

OIKE

## RAW SEQUENCE LISTING

DATE: 06/28/2001

PATENT APPLICATION: US/09/879,792

TIME: 10:53:43

Input Set : A:\02973.00035 sequence listing.txt

Output Set: N:\CRF3\06282001\I879792.raw

4 <110> APPLICANT: Xiao, Yonghong  
 5 Gedrich, Richard  
 7 <120> TITLE OF INVENTION: Regulation of Human Transmembrane Serine  
 8 Protease  
 10 <130> FILE REFERENCE: 02973.00035  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/879,792  
 C--> 12 <141> CURRENT FILING DATE: 2001-06-13  
 12 <150> PRIOR APPLICATION NUMBER: US 60/211,224  
 13 <151> PRIOR FILING DATE: 2000-06-13  
 15 <150> PRIOR APPLICATION NUMBER: US 60/283,353  
 16 <151> PRIOR FILING DATE: 2001-04-13  
 18 <150> PRIOR APPLICATION NUMBER: US 60/283,648  
 19 <151> PRIOR FILING DATE: 2001-04-16  
 21 <150> PRIOR APPLICATION NUMBER: PCT \_\_\_\_\_ (Docket No. LIO-81-WO)  
 22 <151> PRIOR FILING DATE: 2001-06-12  
 24 <160> NUMBER OF SEQ ID NOS: 36  
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 402  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: Homo sapiens  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: misc\_feature  
 35 <222> LOCATION: (1)...(402)  
 36 <223> OTHER INFORMATION: n = A,T,C or G  
 38 <400> SEQUENCE: 1  
 39 aatgcccttc ccagcgggtat atctccctcc agtgttccca ctgcggactg agggccatga 60  
 40 ccgggcggat cgtgggaggg gcgctggcct cggatagcaa gtggccttgg caagtgaagg 120  
 41 tgcacttcgg caccaccac atctgtggag gcacgtcat tgacgccag tgggtgtca 180  
 W--> 42 ctncgcacca ctgttcttc gtgnaccggg gagaaggctc tggagggtg gaagggtgtac 240  
 43 gcgggcacca gcaacctgca ccagttgcct gaggcagcct ccattgccga gatcatcatc 300  
 44 aacagcaatt acaccgatga ggaggacgac tatgacatcg ccctcatgcy gctgttcaag 360  
 W--> 45 ncccttgacc ctgttcgggt gaggaattt tgcatttccc gt 402  
 47 <210> SEQ ID NO: 2  
 48 <211> LENGTH: 285  
 49 <212> TYPE: DNA  
 50 <213> ORGANISM: Homo sapiens  
 52 <400> SEQUENCE: 2  
 53 ccatgaccgg gcggtatcgtg ggagggggcg tggcctcgga tagcaagtgg ccttggcaag 60  
 54 tgagtctgca ctctggcacc acccatctct gtggaggcac gtcattgac gccagtgagg 120  
 55 tgetcactgc cggccactgc ttcttcgtga cccgggagaa ggtcctggag ggctggaagg 180  
 56 tgtacgggg caccagcaac ctgcaccagt tgcttgaggc agcctccatt gccgagatca 240  
 57 tcatcaacag caattacacc gatgaggagg acgactatga catcg 285  
 59 <210> SEQ ID NO: 3  
 60 <211> LENGTH: 600  
 61 <212> TYPE: DNA  
 62 <213> ORGANISM: Homo sapiens

ENTERED

See p.5

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64 <220> FEATURE:
65 <221> NAME/KEY: misc_feature
66 <222> LOCATION: (1)...(600) /
67 <223> OTHER INFORMATION: n = A,T,C or G
69 <400> SEQUENCE: 3
70 gagggctgga aggtgtacgc gggcaccagc aacctgcacc agttgcctga ggcagcctcc      60
71 attgccgaga tcatcatcaa cagcaattac accgatgagg aggacgacta tgacatcgcc      120
72 ctcatgcggc tgtccaagcc cctgaccctg tccggtgagg gaatctgcac tccccgtctt      180
73 cctgcccccc agccccagca ccctctgcag ccctcgcaact tgtcagcatc tgtcaactca      240
74 tatccggggc ccaaagcttc tgcagggcag aagtcaaaga ctcttaaaga tccttacatg      300
75 gaacacttct gttttataat tagggaaact gaagcccaag ggttataaat aagtttgctc      360
76 caaatgacac atctcacatt acaaattgat gacggagtca gggcttgggt actgatctta      420
77 atcaatagat tgaattcttt cactggtatt aactgagcac ctagggggcca aacgctatgg      480
78 taggcatttc acacatatga ttctatttac tcttcacaac caacctgtg gagcaggcac      540
W--> 79 tattattaac ttcatttgac atatgangaa atggagcttt acagagagat aattacctga      600
81 <210> SEQ ID NO: 4
82 <211> LENGTH: 591
83 <212> TYPE: DNA
84 <213> ORGANISM: Homo sapiens
86 <220> FEATURE:
87 <221> NAME/KEY: misc_feature
88 <222> LOCATION: (1)...(591) /
89 <223> OTHER INFORMATION: n = A,T,C or G
91 <400> SEQUENCE: 4
92 gagggctgga aggtgtacgc gggcaccagc aacctgcacc agttgcctga ggcagcctcc      60
93 attgccgaga tcatcatcaa cagcaattac accgatgagg aggacgacta tgacatcgcc      120
94 ctcatgcggc tgtccaagcc cctgaccctg tccggtgagg gaatctgcac tccccgtctt      180
95 cctgcccccc agccccagca ccctctgcag ccctcgcaact tgtcagcatc tgtcaactca      240
96 tatccggggc ccaaagcttc tgcagggcag aagtcaaaga ctcttaaaga tccttacatg      300
97 gaacacttct gttttataat tagggaaact gaagcccaag ggttataaat aagtttgctc      360
98 caaatgacac atctcacatt acaaattgat gacggagtca gggcttgggt actgatctta      420
99 atcaatagat tgaattcttt cactggtatt aactgagcac ctagggggcca aacgctatgg      480
W--> 100 taggcatttc acacatatga ttctatttac tcttcacaac caacctgtg gagcangcac      540
W--> 101 tattattaac ttcatttgac atatgangaa atggagcttt acagagagat a          591
103 <210> SEQ ID NO: 5
104 <211> LENGTH: 286
105 <212> TYPE: DNA
106 <213> ORGANISM: Homo sapiens
108 <400> SEQUENCE: 5
109 gcgatgtcat agtcgtcctc ctcatcggcg taattgctgt tgatgatgat ctcggaatg      60
110 gaggtgcct caggcaactg gtgcaggttg ctggtgcccg cgtacacctt ccagccctcc      120
111 aagaccttct cccgggtcac gaagaagcag tgggcggcag tgagcaccga ctgggcgtca      180
112 atgagcgtgc ctccacagat gtgggtggtg ccgaagtgtc gactcacttg ccaaggccac      240
113 ttgctattcg aggccagcgc cccttccacg attcgcccgg tcatgg          286
115 <210> SEQ ID NO: 6
116 <211> LENGTH: 384
117 <212> TYPE: DNA
118 <213> ORGANISM: Homo sapiens
120 <400> SEQUENCE: 6

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```

121 gagggctgga aggtgtacgc gggcaccagc aacctgcacc agttgcctga ggagcctcca      60
122 ttgccgagat catcatcaac agcaattaca ccgatgagga ggacgactat gacatcgccc      120
123 tcatgcggct gtccaagccc ctgacctgt ccggtgaggg aatctgcact cccgctctc      180
124 ctgcccccca gccccagcac cctctgcagc cctcgcaact gtcagcatct gtcaactcat      240
125 atccggggccc caaagcttct gcagggcaga agtcaaagac tcttaaagat cttacatgg      300
126 aacacttctg tttataatt agggaaactg aagcccaagg gttataaata agtttgetcc      360
127 aaatgacaca tctcacatta caaa                                     384
129 <210> SEQ ID NO: 7
130 <211> LENGTH: 471
131 <212> TYPE: DNA
132 <213> ORGANISM: Homo sapiens
134 <220> FEATURE:
135 <221> NAME/KEY: misc_feature
136 <222> LOCATION: (1)...(471) /
137 <223> OTHER INFORMATION: n = A,T,C or G
139 <400> SEQUENCE: 7
W--> 140 tttttttttt nttttttttt ttggagcaaa cttatttana acccttgggc ttcagttnc      60
W--> 141 ctaattataa aacagaagtn tnccatgtaa ggncttnaa gagtctttga cttctgccct      120
142 gcagaagctt tggggcccg atatgagttg acagatgctg acaagtgcga gggctgcaga      180
W--> 143 gggtnctggg gctggggggc aggagagcgg ggagtgcaga ttcctcacc ggacagggtc      240
W--> 144 aggggnttgg acagccgcag gagggcgatg tcatagtcgt cctcctcatc ggtgtaatnn      300
W--> 145 ctnttgatga tgatctcggc aatggaggct gcctcaggca actgggtncg ggttctggg      360
W--> 146 tnccncgta acaccttcca gccntccagg nccttttccc gggtcacgaa gaagcagtng      420
W--> 147 ggccgcaatt agcaccact ggggggtcaat gaggtgccn ccacanattt g          471
149 <210> SEQ ID NO: 8
150 <211> LENGTH: 235
151 <212> TYPE: DNA
152 <213> ORGANISM: Homo sapiens
154 <400> SEQUENCE: 8
155 gggctggaag gtgtacgcgg gcaccagcaa cctgcaccag ttgcctgagc agcctccatt      60
156 gccgagatca tcatcaacag caattacacc gatgaggagg acgactatga catcgccctc      120
157 atgcggctgt ccaagccctt gacctgtcc ggtgaggaa tctgcactcc ccgtctcct      180
158 gccccccagc cccagcacc tctgcagccc tcgcacttgt cagcatctgt caact          235
160 <210> SEQ ID NO: 9
161 <211> LENGTH: 19
162 <212> TYPE: DNA
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 9
166 ctgccagcag ctgggtttc                                     19
168 <210> SEQ ID NO: 10
169 <211> LENGTH: 20
170 <212> TYPE: DNA
171 <213> ORGANISM: Homo sapiens
173 <400> SEQUENCE: 10
174 aggtttcct ggatggtgga                                     20
176 <210> SEQ ID NO: 11
177 <211> LENGTH: 1748
178 <212> TYPE: DNA
179 <213> ORGANISM: Homo sapiens

```

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181 <400> SEQUENCE: 11
182 ctcagagacc atggagaggg acagccaagg gaatgcatct ccagcaagaa caccttcagc      60
183 tggagcatct ccagcccagg catctccagc tgggacacct ccaggccggg catctccagc      120
184 ccaggcatct ccagcccagg catctccagc tgggacacct ccgggccggg catctccagc      180
185 ccaggcatct ccagctggta cacctccagg ccgggcatct ccaggccggg catctccagc      240
186 ccaggcatct ccagcccagg catctccagg tctggcatca ctttccaggt cctcatccgg      300
187 caggtcata tccgccagg cagcctcggg gacaacctcc ccaaccagag tgtaccttgt      360
188 tagagcaaca ccagtggggg ctgtacccat ccgatcatct cctgccagg cagcaccagc      420
189 aaccagggcc accagggaga gccagggtac gagcctgccc aagttcacct ggcgggagg      480
190 ccagaagcag ctaccgctca tgggtgctg gctcctcctc attgccctgg tggtttcgct      540
191 catcactctc ttccagttct ggcaggggcca cacagggtac aggtacaagg agcagaggga      600
192 gagctgtccc aagcacgctg ttctgctgtg cggggtgggt gactgcaagc tgaagagtga      660
193 cgagctgggc tgcgtgaggt ttgactggga caagtctctg cttaaaatct actctgggtc      720
194 ctcccacagc tggcttccca ctgttagcag caactggaat gactcctact cagagaagac      780
195 ctgccagcag ctgggtttcg agagtgtcga ccggacaacc gaggttgccc acagggattt      840
196 tgccaacagc ttctcaatct tgagatacaa ctccaccatc caggaaagcc tccacaggtc      900
197 tgaatgcctt tcccagcggg atatctccct ccagtgttcc cactgcggac tgagggccat      960
198 gaccggggcg atcgtgggag ggcgcgtggc ctcgatagc aagtggcctt ggcaagtga      1020
199 tctgcacttc ggcaccaccc acatctgttg aggcacgctc attgacgcc agtgggtgct      1080
200 cactgccgcc cactgcttct tctgacccg ggagaaggtc ctggagggtc ggaagggtga      1140
201 cgcgggcacc agcaacctgc accagttgcc tgaggcagcc tccattgcc agatcatcat      1200
202 caacagcaat tacaccgatg aggaggacga ctatgacatc gccctcatgc ggctgtccaa      1260
203 gccctgacc ctgtccgctc acatccaccc tgcctgcctc cccatgcatg gacagacctt      1320
204 tagcctcaat gagacctgct ggatcacagg ctttggaag accagggaga cagatgacaa      1380
205 gacatcccc ttctccggg aggtgcaggt caatctcatc gacttcaaga aatgcaatga      1440
206 ctacttggtc tatgacagtt accttaccct aaggatgatg tgtgctggg accttcgtgg      1500
207 gggcagagac tctgccagg gagacagcgg ggggcctctt gtctgtgagc agaacaaccg      1560
208 ctggtacctg gcagggtgta ccagctggg caccggctgt ggccagagaa acaaacctgg      1620
209 tgtgtacacc aaagtgcag aagttcttcc ctggatttac agcaagatgg agagcgaggt      1680
210 gcgattcaga aaatcctaac cagcctctct gctgctctgc acagcaccgg ctgctgtgac      1740
211 tcgagaaa

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213 &lt;210&gt; SEQ ID NO: 12

214 &lt;211&gt; LENGTH: 562

215 &lt;212&gt; TYPE: PRT

216 &lt;213&gt; ORGANISM: Homo sapiens

218 &lt;400&gt; SEQUENCE: 12

```

219 Met Glu Arg Asp Ser His Gly Asn Ala Ser Pro Ala Arg Thr Pro Ser
220 1      5      10      15
221 Ala Gly Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr Pro Pro Gly
222      20      25      30
223 Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly
224      35      40      45
225 Thr Pro Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr
226      50      55      60
227 Pro Pro Gly Arg Ala Ser Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser
228 65      70      75      80
229 Pro Ala Arg Ala Ser Pro Ala Leu Ala Ser Leu Ser Arg Ser Ser Ser
230      85      90      95
231 Gly Arg Ser Ser Ser Ala Arg Ser Ala Ser Val Thr Thr Ser Pro Thr

```

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```

232          100          105          110
233 Arg Val Tyr Leu Val Arg Ala Thr Pro Val Gly Ala Val Pro Ile Arg
234          115          120          125
235 Ser Ser Pro Ala Arg Ser Ala Pro Ala Thr Arg Ala Thr Arg Glu Ser
236          130          135          140
237 Pro Gly Thr Ser Leu Pro Lys Phe Thr Trp Arg Glu Gly Gln Lys Gln
238 145          150          155          160
239 Leu Pro Leu Ile Gly Cys Val Leu Leu Leu Ile Ala Leu Val Val Ser
240          165          170          175
241 Leu Ile Ile Leu Phe Gln Phe Trp Gln Gly His Thr Gly Ile Arg Tyr
242          180          185          190
243 Lys Glu Gln Arg Glu Ser Cys Pro Lys His Ala Val Arg Cys Asp Gly
244          195          200          205
245 Val Val Asp Cys Lys Leu Lys Ser Asp Glu Leu Gly Cys Val Arg Phe
246          210          215          220
247 Asp Trp Asp Lys Ser Leu Leu Lys Ile Tyr Ser Gly Ser Ser His Gln
248 225          230          235          240
249 Trp Leu Pro Ile Cys Ser Ser Asn Trp Asn Asp Ser Tyr Ser Glu Lys
250          245          250          255
251 Thr Cys Gln Gln Leu Gly Phe Glu Ser Ala His Arg Thr Thr Glu Val
252          260          265          270
253 Ala His Arg Asp Phe Ala Asn Ser Phe Ser Ile Leu Arg Tyr Asn Ser
254          275          280          285
255 Thr Ile Gln Glu Ser Leu His Arg Ser Glu Cys Pro Ser Gln Arg Tyr
256          290          295          300
257 Ile Ser Leu Gln Cys Ser His Cys Gly Leu Arg Ala Met Thr Gly Arg
258 305          310          315          320
259 Ile Val Gly Gly Ala Leu Ala Ser Asp Ser Lys Trp Pro Trp Gln Val
260          325          330          335
261 Ser Leu His Phe Gly Thr Thr His Ile Cys Gly Gly Thr Leu Ile Asp
262          340          345          350
263 Ala Gln Trp Val Leu Thr Ala Ala His Cys Phe Phe Val Thr Arg Glu
264          355          360          365
265 Lys Val Leu Glu Gly Trp Lys Val Tyr Ala Gly Thr Ser Asn Leu His
266          370          375          380
267 Gln Leu Pro Glu Ala Ala Ser Ile Ala Glu Ile Ile Ile Asn Ser Asn
268 385          390          395          400
269 Tyr Thr Asp Glu Glu Asp Asp Tyr Asp Ile Ala Leu Met Arg Leu Ser
270          405          410          415
271 Lys Pro Leu Thr Leu Ser Ala His Ile His Pro Ala Cys Leu Pro Met
272          420          425          430
273 His Gly Gln Thr Phe Ser Leu Asn Glu Thr Cys Trp Ile Thr Gly Phe
274          435          440          445
275 Gly Lys Thr Arg Glu Thr Asp Asp Lys Thr Ser Pro Phe Leu Arg Glu
276          450          455          460
277 Val Gln Val Asn Leu Ile Asp Phe Lys Lys Cys Asn Asp Tyr Leu Val
278 465          470          475          480
279 Tyr Asp Ser Tyr Leu Thr Pro Arg Met Met Cys Ala Gly Asp Leu Arg
280          485          490          495

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\02973.00035 sequence listing.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:45 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:145 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35